

## WEST Search History

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DATE: Wednesday, August 11, 2004

<b>Hide?</b>	<b>Set Name</b>	<b>Query</b>	<b>Hit Count</b>
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L4	L2 and cinnamomensis	34
<input type="checkbox"/>	L3	monensi\$ same (polyketide adj2 (synthase or synthetase))	133
<input type="checkbox"/>	L2	monensi\$ and (polyketide adj2 (synthase or synthetase))	169
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L1	monensi\$ and (polyketide adj2 (synthase or synthetase))	64

END OF SEARCH HISTORY

09/980217  
STN Search Summary

=> d his

FILE 'REGISTRY' ENTERED AT 12:19:23 ON 11 AUG 2004  
L1 1 S 17090-79-8/RN  
FILE 'CAPLUS' ENTERED AT 12:19:55 ON 11 AUG 2004  
L2 2407 S L1  
L3 7 S L2 AND (POLYKETIDE (2W) (SYNTHASE OR SYNTHETASE))  
L4 79 S L1 AND CINNAMONENSIS  
L5 11 S L4 AND (GENE OR ENZYME OR NUCLEOTIDE)  
L6 5 S L5 NOT L3

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 17090-79-8 REGISTRY  
CN Monensin (9CI) (CA INDEX NAME)  
OTHER CA INDEX NAMES:  
CN 1,6-Dioxaspiro[4.5]decane, monensin deriv.  
CN 1,6-Dioxaspiro[4.5]decane-7-butyric acid, 2-[5-ethyltetrahydro-5-[tetrahydro-3-methyl-5-[tetrahydro-6-hydroxy-6-(hydroxymethyl)-3,5-dimethyl-2H-pyran-2-yl]-2-furyl]-2-furyl]-9-hydroxy-.beta.-methoxy-.alpha.,.gamma.,2,8-tetramethyl- (8CI)  
OTHER NAMES:  
CN A 3823A  
CN Elancoban  
CN Monelan  
CN Monensic acid  
CN Monensin A  
CN Stereoisomer of 2-[2-ethyloctahydro-3'-methyl-5'-[tetrahydro-6-hydroxy-6-(hydroxymethyl)-3,5-dimethyl-2H-pyran-2-yl][2,2'-bifuran]-5-yl]-9-hydroxy-.beta.-methoxy-.alpha.,.gamma.,2,8-tetramethyl-1,6-dioxaspiro[4.5]decane-7-butanoic acid  
DR 1392-52-5  
MF C36 H62 O11

L3 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2003:826990 CAPLUS  
TI Intermediates released from a polyether-producing polyketide synthase provide insight into the mechanism of oxidative cyclization  
AU Hughes-Thomas, Zoe A.; Stark, B. W.; Boehm, Ines U.; Staunton, James; Leadlay, Peter F.  
SO Angewandte Chemie, International Edition (2003), 42(37), 4475-4478

L3 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2003:775709 CAPLUS  
TI Analysis of the biosynthetic gene cluster for the polyether antibiotic monensin in Streptomyces cinnamomensis and evidence for the role of monB and monC genes in oxidative cyclization  
AU Oliynyk, Markiyana; Stark, Christian B. W.; Bhatt, Apoorva; Jones, Michelle A.; Hughes-Thomas, Zoe A.; Wilkinson, Christopher; Oliynyk, Zoryana; Demydchuk, Yuliya; Staunton, James; Leadlay, Peter F.  
SO Molecular Microbiology (2003), 49(5), 1179-1190

L3 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2002:17941 CAPLUS  
 TI Engineering of complex polyketide biosynthesis - insights from sequencing  
 of the monensin biosynthetic gene cluster  
 AU Leadlay, P. F.; Staunton, J.; Oliynyk, M.; Bisang, C.; Cortes, J.; Frost,  
 E.; Hughes-Thomas, Z. A.; Jones, M. A.; Kendrew, S. G.; Lester, J. B.;  
 Long, P. F.; McArthur, H. A. I.; McCormick, E. L.; Oliynyk, Z.; Stark, C.  
 B. W.; Wilkinson, C. J.  
 SO Journal of Industrial Microbiology & Biotechnology (2001), 27(6), 360-367

L3 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2001:693525 CAPLUS  
 TI A type I polyketide synthase for monensin biosynthesis  
 and the corresponding gene cluster of Streptomyces cinnamomensis and the  
 engineering of novel polyketide synthases  
 IN Leadlay, Peter Francis; Staunton, James; Oliynyk, Marko  

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----
PI WO 2001068867	A1	20010920	WO 2000-GB2072	20000530
EP 1183369	A1	20020306	EP 2000-931459	20000530
PRAI GB 1999-12563	A	19990528		
WO 2000-GB2072	W	20000530		

L3 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2000:15378 CAPLUS  
 TI Functional domains of polyketide synthetases and their  
 use in the generation of novel synthetases and novel macrolide antibiotics  
 IN Leadlay, Peter Francis; Staunton, James; Cortes, Jesus; McArthur, Hamish  
 Alastair Irvine  

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----
PI WO 2000000618	A2	20000106	WO 1999-GB2044	19990629
WO 2000000618	A3	20000427		
AU 9945247	A1	20000117	AU 1999-45247	19990629
AU 763230	B2	20030717		
BR 9911712	A	20010320	BR 1999-11712	19990629
EP 1090123	A2	20010411	EP 1999-928128	19990629
TR 200003770	T2	20010420	TR 2000-200003770	19990629
TR 200003771	T2	20011022	TR 2000-200003771	19990629
JP 2002519032	T2	20020702	JP 2000-557371	19990629
NZ 509600	A	20040326	NZ 1999-509600	19990629
PRAI GB 1998-14006	A	19980629		
WO 1999-GB2044	W	19990629		

L3 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1998:65985 CAPLUS  
 TI Polyketides and their synthesis in Streptomyces strains transformed with  
 hybrid type I polyketide synthases  
 IN Leadlay, Peter Francis; Staunton, James; Cortes, Jesus  

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----
PI WO 9801546	A2	19980115	WO 1997-GB1819	19970704
WO 9801546	A3	19980409		
CA 2259420	AA	19980115	CA 1997-2259420	19970704
CA 2259463	AA	19980115	CA 1997-2259463	19970704
AU 9734514	A1	19980202	AU 1997-34514	19970704
AU 731654	B2	20010405		

EP 910633	A2	19990428	EP 1997-930631	19970704
CN 1229438	A	19990922	CN 1997-197649	19970704
JP 2000511063	T2	20000829	JP 1998-504933	19970704
WO 9854308	A2	19981203	WO 1998-GB1559	19980528
WO 9854308	A3	19990408		
AU 9876661	A1	19981230	AU 1998-76661	19980528
EP 983348	A2	20000308	EP 1998-924463	19980528
KR 2000023579	A	20000425	KR 1999-700024	19990105
US 2002004487	A1	20020110	US 2001-896357	20010629
US 6437151	B2	20020820		
US 2003104585	A1	20030605	US 2002-307595	20021202
PRAI GB 1996-14189	A	19960705		
US 1996-24188P	P	19960819		
GB 1997-10962	A	19970528		
WO 1997-GB1819	W	19970704		
WO 1998-GB1559	W	19980528		
US 1999-214454	A3	19990916		
US 1999-424751	A1	19991129		

L3 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1987:170050 CAPLUS  
 TI Homology between *Streptomyces* genes coding for synthesis of different polyketides used to clone antibiotic biosynthetic genes  
 AU Malpartida, F.; Hallam, S. E.; Kieser, H. M.; Motamedi, H.; Hutchinson, C. R.; Butler, M. J.; Sugden, D. A.; Warren, M.; McKillop, C.; et al.  
 SO Nature (London, United Kingdom) (1987), 325(6107), 818-21

L6 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2001:183742 CAPLUS  
 TI MeaA, a putative coenzyme B12-dependent mutase, provides methylmalonyl coenzyme A for monensin biosynthesis in *Streptomyces cinnamonensis*  
 AU Zhang, Weiwen; Reynolds, Kevin A.  
 SO Journal of Bacteriology (2001), 183(6), 2071-2080

L6 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2000:291460 CAPLUS  
 TI Molecular analysis and heterologous expression of the gene encoding methylmalonyl-coenzyme A mutase from rifamycin SV-producing strain *Amycolatopsis mediterranei* U32  
 AU Zhang, Weiwen; Yang, Ling; Jiang, Weihong; Zhao, Guoping; Yang, Yinliu; Chiao, Juishen  
 SO Applied Biochemistry and Biotechnology (1999), 82(3), 209-225

L6 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1999:713971 CAPLUS  
 TI Role of crotonyl coenzyme A reductase in determining the ratio of polyketides monensin A and B produced by *Streptomyces cinnamonensis*  
 AU Liu, Haibin; Reynolds, Kevin A.  
 SO Journal of Bacteriology (1999), 181(21), 6806-6813

L6 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1999:194858 CAPLUS  
 TI Overproduction of 2-ketoisovalerate and monensin production by regulatory mutants of *Streptomyces cinnamonensis* resistant to 2-ketobutyrate and amino acids  
 AU Pospisil, S.; Kopecky, J.; Prikrylova, V.; Spizek, J.  
 SO FEMS Microbiology Letters (1999), 172(2), 197-204

# SEQ SEARCH SUMMARY

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 19:13:20 ; Search time 44373 Seconds  
(without alignments)  
11835.746 Million cell updates/sec

Title: US-09-980-217-2 COPY 12448\_24564 = monAIV coding region  
Perfect score: 12117  
Sequence: 1 atgtcgtgagtgctgaagagtc.....acaaagaactgggtgtgtga 12117

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	12117	100.0	30000	6	AX250262	Sequence
2	12117	100.0	103450	1	AF440781	Streptomy
3	4440.6	36.6	30000	6	AX250263	Sequence
4	3934	32.5	132544	1	AF521085	Streptomy
5	3580.8	29.6	30000	6	AX250261	Sequence
6	3485.6	28.8	113193	1	AF357202	Streptomy
7	3485.6	28.8	113193	6	AX703543	Sequence
8	3228.6	26.6	65140	6	AX211705	Sequence
9	3228.6	26.6	123580	1	AF263912	Streptomy
10	3228.6	26.6	125401	6	AX211739	Sequence
c 11	3009.8	24.8	132544	1	AF521085	Streptomy
c 12	2976.2	24.6	104326	1	AB070940	Streptomy
13	2976.2	24.6	281450	1	AP005032	Streptomy
14	2803.2	23.1	20394	1	SNA132222	Streptomy
15	2803.2	23.1	20394	6	AX067996	Sequence
c 16	2803.2	23.1	84985	1	SNA278573	Streptomy
c 17	2786.4	23.0	138203	1	AY310323	Streptomy
c 18	2727.4	22.5	290850	1	SCO939127	Streptomy
19	2684.6	22.2	78210	1	AB070949	Streptomy
c 20	2679.2	22.1	300425	1	AP005022	Streptomy
21	2670.8	22.0	104326	1	AB070940	Streptomy
c 22	2670.8	22.0	320150	1	AP005033	Streptomy
23	2666.8	22.0	27541	6	AX211706	Sequence
24	2536.4	20.9	75236	6	AX600586	Sequence
c 25	2506.4	20.7	30000	6	AX250263	Sequence
c 26	2506.4	20.7	103450	1	AF440781	Streptomy
27	2473.6	20.4	69644	1	AY179507	Streptomy
28	2454.2	20.3	50000	6	AX089417	Sequence
29	2454.2	20.3	50000	6	AX089420	Sequence
30	2454.2	20.3	80161	1	AY007564	Saccharop
31	2454.2	20.3	80161	6	AR165018	Sequence
32	2454.2	20.3	80161	6	AR281866	Sequence
33	2454.2	20.3	80161	6	BD137649	Biosynthe

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 20:41:04 ; Search time 3880 Seconds  
(without alignments)  
13266.860 Million cell updates/sec

Title: US-09-980-217-2\_COPY\_12448\_24564  
Perfect score: 12117  
Sequence: 1 atgtcgagtgtgctgaagagtc.....acaaagaactgggtgtgtga 12117  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3373863 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 6747726  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match Length DB	ID		
	1	12117	100.0 103599	4	ABX04971	Abx04971 S. cinnam
	2	3485.6	28.8 113193	7	AAD54645	Aad54645 Streptomy
	3	3228.6	26.6 65140	4	AAD17184	Aad17184 Streptomy
	4	3228.6	26.6 125401	4	AAD17186	Aad17186 Streptomy
	5	2803.2	23.1 20394	4	AAF24892	Aaf24892 Pimaricin
	6	2666.8	22.0 27541	4	AAD17185	Aad17185 Streptomy
	7	2536.4	20.9 75236	7	ABV75557	Abv75557 Saccharop
c	8	2506.4	20.7 103599	4	ABX04971	Abx04971 S. cinnam
	9	2454.2	20.3 50000	4	AAF88313	Aaf88313 S. spinos
	10	2454.2	20.3 50000	4	AAF88316	Aaf88316 S. spinos
	11	2454.2	20.3 80161	2	AAZ21501	Aaz21501 DNA fragm
	12	2454	20.3 16767	4	AAF88339	Aaf88339 S. spinos
	13	2386.8	19.7 15872	3	AAZ87283	Aaz87283 S. venezu
	14	2375.6	19.6 53789	2	AAV21187	Aav21187 Amycolato
	15	2367.6	19.5 15872	2	AAT68715	Aat68715 Streptomy
	16	2110.4	17.4 67251	9	ADC26995	Adc26995 Sorangium

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 20:38:04 ; Search time 830 Seconds  
(without alignments)  
8101.614 Million cell updates/sec

Title: US-09-980-217-2\_COPY\_12448\_24564  
Perfect score: 12117  
Sequence: 1 atgtcgagtgtctgaagagtc.....acaaagaactgggtgtgtga 12117  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 682709 seqs, 277475446 residues  
Total number of hits satisfying chosen parameters: 1365418  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2454.2	20.3	80161	3	US-09-036-987A-1	Sequence 1, Appli
2	2454.2	20.3	80161	3	US-09-370-700-1	Sequence 1, Appli
3	2454.2	20.3	80161	4	US-09-603-207-1	Sequence 1, Appli
4	2386.8	19.7	15872	3	US-09-105-537-1	Sequence 1, Appli
5	2386.8	19.7	15872	4	US-09-091-609-1	Sequence 1, Appli
6	2386.8	19.7	15872	4	US-09-091-609-3	Sequence 3, Appli
7	2030.2	16.8	44377	2	US-08-804-227C-7	Sequence 7, Appli
8	2030.2	16.8	44377	2	US-08-804-198-1	Sequence 1, Appli
9	1999	16.5	50937	3	US-09-428-517-1	Sequence 1, Appli
c 10	1984.6	16.4	77536	4	US-09-410-551B-1	Sequence 1, Appli
11	1967.2	16.2	43280	2	US-08-804-227C-1	Sequence 1, Appli
12	1965.8	16.2	33529	3	US-09-144-085-3	Sequence 3, Appli
c 13	1954	16.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	1943	16.0	38506	3	US-09-320-878-19	Sequence 19, Appl
15	1943	16.0	38506	4	US-09-141-908-1	Sequence 1, Appli
16	1943	16.0	38506	4	US-09-657-440-19	Sequence 19, Appl
17	1939.4	16.0	11220	3	US-09-105-537-32	Sequence 32, Appl
18	1939.4	16.0	36778	3	US-09-105-537-5	Sequence 5, Appli
c 19	1933.8	16.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
20	1854	15.3	20235	1	US-07-642-734C-3	Sequence 3, Appli



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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 20:43:23 ; Search time 4567 Seconds  
(without alignments)  
12154.381 Million cell updates/sec

Title: US-09-980-217-2\_COPY\_12448\_24564

Perfect score: 12117

Sequence: 1 atgtcgagtgtgaagagtc.....acaaagaactgggtgtgtga 12117

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		%							
Result	Query								
No.	Score	Match	Length	DB	ID	Description			
c	1	2976.2	24.6	125746	15	US-10-156-761-15102	Sequence 15102, A		
	2	2976.2	24.6	9025608	15	US-10-156-761-1	Sequence 1, Appli		
	3	2963.2	24.5	11910	15	US-10-156-761-2879	Sequence 2879, Ap		
	4	2679.2	22.1	23238	15	US-10-156-761-415	Sequence 415, App		
	5	2679.2	22.1	100000	15	US-10-156-761-15103	Sequence 15103, A		
c	6	2679.2	22.1	9025608	15	US-10-156-761-1	Sequence 1, Appli		
	7	2670.8	22.0	125746	15	US-10-156-761-15102	Sequence 15102, A		